





DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE UV excision repair protein RAD23 homolog A (HHR23A).  
 GN RAD23A.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=94222030; PubMed=8168482;  
 RA Mesutani C., Sugawara K., Yanagisawa J., Sonoyama T., Uj M.,  
 RA Enomoto T., Takio K., Tanaka K., van der Spek P.J., Bootsma D.,  
 RA Hoeljmakers J.H.J., Hanaoka F.;  
 RT Purification and cloning of a nucleotide excision repair complex  
 RT involving the xeroderma pigmentosum group C protein and a human  
 RT homologue of yeast Rad23.";  
 RL EMBO J. 13:1831-1843(1994).  
 RP SEQUENCE FROM N.A.  
 RA Lamedin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP STRUCTURE BY NMR OF 319-363.  
 RX MEDLINE=99061330; PubMed=9846873;  
 RA Dieckmann T., Withers-Ward E.S., Jarosinski M.A., Liu C.F.,  
 RA Chen I.S.Y., Felgon J.;  
 RT "Structure of a human DNA repair protein UBA domain that interacts  
 RT with HIV-1 Vpr.";  
 RL Nat. Struct. Biol. 5:1042-1047(1998).  
 RN [4]  
 RP STRUCTURE BY NMR OF 319-363.  
 RX MEDLINE=20541363; PubMed=11087358;  
 RA Withers-Ward E.S., Mueller T.D., Chen I.S.Y., Felgon J.;  
 RT "Biochemical and structural analysis of the interaction between the  
 RT UBA(2) domain of the DNA repair protein HHR23A and HIV-1 Vpr.";  
 RL Biochemistry 39:14103-14112(2000).  
 CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.  
 CC Postreplication repair functions in gap-filling of a daughter  
 CC strand on replication of damaged DNA (Potential).  
 CC -1- SUBUNIT: Interacts with MJD.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- DOMAIN: The ubiquitin-like domain mediates interaction with MJD.  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: D12335; BAA04767.1; -;  
 DR EMBL: AD000092; AAB51177.1; -;  
 DR PDB: 1DV0; 11-FEB-00.  
 DR Genew; HGNC:9812; RAD23A.  
 DR MIM: 600061; -;  
 DR InterPro: IPR004806; Rad23.  
 DR InterPro: IPR000449; UBA\_domain.  
 DR InterPro: IPR000626; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR Pfam: PF00627; UBA; 2.  
 DR SMART: SM00165; UBA; 2.  
 DR SMART: SM00213; UBO; 1.  
 DR TRIGRAMS: TIGR00601; Rad23; 1.  
 DR PROSITE: PS5003; UBIQUITIN\_2; 1.  
 DR DNA damage; DNA repair; Nuclear protein; 3D-structure.  
 KW DOMAIN 1 81 UBIQUITIN-LIKE.  
 FT SEQUENCE 363 AA; 39609 MW; C4E47E9313BB47B5 CRC64;  
 Query Match 31.6%; Score 603.5; DB 1; Length 363;

Best Local Similarity 33.4%; Pred. No. 1e-31;  
 Matches 133; Conservative 88; Mismatches 106; Indels 71; Gaps 8;  
 QY 3 LTVKTLKGTHEIRYQPDITIAVKKNEEIOGKSYWPGQGLIFNKVKLKDSELEEN 62  
 Db 5 ITLTKLQOQTRKIRKEPEETVKLKEIEAKGRDAFPAQOKLIYAKLISDDVPINDY 64  
 QY 63 RVNEDGLVWMLSKGTSGSTGSSSHSNTPARQAPPLPAQAPQAPVAPIT----- 117  
 Db 65 RIDENKFFVAVVT--KTRAGOGTS-----APPEASPTAPPESTSFPPAPSGMSH 114  
 QY 118 -----TSQPECLPAQAPNT-----HDNAASNLISGRVDTITNLMEMG 156  
 Db 115 PPAAREDKSPSEESAPPTSPESVSGVSSSGREEDASTLVYGSYEFTMLEISMVG 174  
 QY 157 GGSMDKDVORALRAVYVAVYVAVYVAVYVAVYVAVYVAVYVAVYVAVYVAVYVAVY 216  
 Db 175 ---YERERVAALRASTYNNPRAVEYLLTGTP-----GSPPEGSGVQESQVS 219  
 QY 217 GIPNTAPLDLPQGCASNAGGAGGGLDPLFRNNDPQVAVREMYHTNPQILQPMLELSKQ 276  
 Db 220 EQPATE-----AAGENPLEFLRDQPFQMRQVYIQNPALLPALLOQLQGE 265  
 QY 277 NPQILRIEENHDEFLQLNEP-----FEGEGDPLDQPEDEMPHAIISTVPEQEAIG 330  
 Db 266 NPQLQOQISRHQEQPIQMLNEPPEGLADISDEGEVGAIGEAQPMNYIQVTPQEKKAIE 325  
 QY 331 RLESMPDRARVIEAFACDRNEELANVYLEHAGEED 368  
 Db 326 RLKALGPESLVIOAYFACENENLEANPLLSQNFDE 363  
 RESULT 4  
 R23A\_MOUSE  
 ID R23A\_MOUSE STANDARD; PRT; 363 AA.  
 AC P54726;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE UV excision repair protein RAD23 homolog A (HHR23A).  
 GN RAD23A OR HHR23A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Testis;  
 RX MEDLINE=96403997; PubMed=8808275;  
 RA van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,  
 RA Hagemeijer A., Bootsma D., Hoeljmakers J.H.J.;  
 RT "Cloning, comparative mapping, and RNA expression of the mouse  
 RT homologues of the Saccharomyces cerevisiae nucleotide excision repair  
 RT gene RAD23.";  
 RL Genomics 31:20-27(1996).  
 CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.  
 CC Postreplication repair functions in gap-filling of a daughter  
 CC strand on replication of damaged DNA (Potential).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: X92410; CAA63145.1; -;  
 DR HSSP: P54725; 1DV0.  
 DR MGD; MGI:105126; Rad23a.

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DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin_1.
DR Pfam: PF00627; UBA; 2.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBA; 2.
DR TIGRFAMs: TIGR00601; Rad23; 1.
DR PROSITE: PS50053; Ubiquitin_2; 1.
DR DNA damage; DNA repair; Nuclear protein.
KW UBIQUITIN-LIKE.
FT DOMAIN 1 79
SQ SEQUENCE 363 AA; 39769 MW; 67EAB96EEBA5C03 CRC64;

Query Match 31.3%; Score 597.5; DB 1; Length 363;
Best Local Similarity 33.7%; Pred. No. 2,4e-31;
Matches 136; Conservative 84; Mismatches 101; Indels 83; Gaps 11;

OY 3 LKVTIKGTHFEIRVOQNDITMAVKKNIIEIGKDSYPMGQQLITNGVKLKESTLEEN 62
DB 5 IRLTKIQOQTFKIRMPDETIVKYLKEIKERKQDAFVPAQGLITAGKILSDVPTRDY 64
OY 63 KVNEDGFLVYMLSKGTSSTGTSSQSHNTPATROAPLEAPQAPQAP--PVAPI---- 116
DB 65 HIDEKNEVYVYTKAK--AGGGIS-----APPEASPTAVPESTPEPPVLASG 110
OY 117 -----TTSOPEGLPAQAPNT-----HDNAASMLSGRNVTITINOL 152
DB 111 MSHPPPTSSSEDSKSPSESTTTTSSPESISGVSPPSSSGREEDAASTLVGSEYETMLTEL 170
OY 153 MEMGSGMDKDKVQALRAAYNPERAVELYSGIPVTAIEINAVIGCGANTDRA--PT 210
DB 171 MSGG---YERERVVALRASYNPHRAVEYLITGIGSP---PEIG-SYQEQRAEQA 223
OY 211 GEAGLSGIDPNTAPLDLFPQAGSAGGAGGCPDLFLRNPQFAVREMYHTNPOLLQPM 270
DB 224 TEA-----ACENPLEFLRDQPFQGNMQVYQIONFALPALL 259
OY 271 VELSKRONPOLRLIEHNDEFLQINEP-----FEGGSGDFLDQEEDEMPAIVTPE 324
DB 260 QOQGGQNPOLLQOISRHOQFOTMLNEPGEELADISDVGEGVAGIEAPQMYTQIVTQ 319
OY 325 EDEATIGRLSMGFRARVIEAFACDRNEELNANYLLEHAHEED 368
DB 320 EKEAIEIRLAKLGPESLVIQAVFACKENKNIANFLLSQNFDE 363

RESULT 5
RH23_SCHPO
ID RH23_SCHPO STANDARD; PRT: 368 AA.
AC 074803;
DR 15-JUN-2002 (Rel. 41, Created)
DR 15-JUN-2002 (Rel. 41, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE UV excision repair protein rhp23 (RAD23 homolog).
GN RHP23 OR SPBC2D10.12.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC STRAIN=SP23;
RA PubMed=11788722;
RA Elder R.T., Song X.-Q., Chen M., Hopkins K.M., Lieberman H.B.,
RA Zhao Y.;
RA "Involvement of rhp23, a Schizosaccharomyces pombe homolog of the
RT human HHR23A and Saccharomyces cerevisiae RAD23 nucleotide excision
RT repair genes, in cell cycle control and protein ubiquitination.";
RL Nucleic Acids Res. 30:561-591(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
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RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Meestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnardt H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandut R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [3]
RP CHARACTERIZATION.
RX PubMed=10652237;
RA Lombaerts M., Goeloe J.L., den Dulk H., Brandsma J.A., Brouwer J.;
RT "Identification and characterization of the rhp23(+) DNA repair gene
RT in Schizosaccharomyces pombe.";
RL Biochem. Biophys. Res. Commun. 268:210-215(2000).
CC -!- FUNCTION: Involved in postreplication repair of UV-damaged DNA.
CC Postreplication repair functions in gap-filling of a daughter
CC strand on replication of damaged DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC
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CC -----
DR EMBL: AF174293; AAD51975.1; -.
DR EMBL: AL031788; CAA21170.1; -.
DR HSSP: P54725; IDVO.
DR InterPro: IPR000449; UBA.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin_1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBA; 2.
DR PROSITE: PS50053; Ubiquitin_2; 1.
DR DNA damage; DNA repair; Nuclear protein.
FT DOMAIN 1 77
FT DOMAIN 119 122
FT DOMAIN 205 208
FT POLY-ALA.
FT POLY-GLN.
SQ SEQUENCE 368 AA; 40135 MW; 5CB75EB7E190BED4 CRC64;

Query Match 29.4%; Score 561.5; DB 1; Length 368;
Best Local Similarity 36.0%; Pred. No. 4,9e-29;
Matches 142; Conservative 70; Mismatches 127; Indels 55; Gaps 12;

OY 1 MKLYVTKGTHFEIRVOQNDITMAVKKNIIEIGKDSYPMGQQLITNGVKLKESTLE 60
DB 1 MNLTFRKNIQOQKFVIVSDVADTKISELK--EKIQQGNVEVERKULIYSGRLADKTYG 58
OY 61 ENKVNEDGFLVYMLSKGTSSTGTSSQSHNTPATROAPLEAPQAPQAPVAPI--TT 118
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Db 59 EYKEDDFYCMVSRKSTSTSPKSA---SPAPN--PAPVPEKKEVPSSTVVEST 112
QY 119 SOPEGLPAQPNTHDNAASN-----LISGRNVDTIINQIMMGSGWMDKDYORALR 170
Db 113 STGTOTVAAPSPNDTATSPAPIDANTLVAGNRNAVEMVMG---YRSEVERMR 169
QY 171 AAYNPERAVEYLSGIP-----VTAEIAPVIGGANTTDRAPTGAGLSIPNAPL 224
Db 170 AAFNNPRAVEYLTGIPEDILNRRESEAAALAAQOQSALAPSTG-----QPA 221
QY 225 DLPEQGA-----SNAGGAGGEPDLFLRNPPQFQAVREWHNPQILOPMLVELSKON 277
Db 222 NLEFOALSENENQPSNTVGDPLGLKSTIPQFQOLRQIVQGNPQMLETIIQIGOGD 281
QY 278 POLRLLENNHDEFLQLINEPEFGEGEDFLDQPEDEMPHA---ISVYPERQALGRLES 334
Db 282 PALAQATONPEANFLQLL---AEGAG-----ESALPSCGIQIQTQESSEIDRLCQ 331
QY 335 MGEDRAVIEAFACDRNEELIANYLLEHAGEED 368
Db 332 LGEDRNIVIOAYLACDKNEELIANYLFEHGHSE 365

RESULT 6
RA23_YEAST STANDARD; PRT; 398 AA.
AC P32628;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-1993 (Rel. 27, Last sequence update)
DE UV excision repair protein RAD23.
GN RAD23 OR YEL037C OR SYCP-ORF29.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=94067136; Pubmed=8246991;
RA Watkins J.F., Sung P., Prakash L., Prakash S.;
RT "The Saccharomyces cerevisiae DNA repair gene RAD23 encodes a nuclear
RT protein containing a ubiquitin-like domain required for biological
RT function."
RL Mol. Cell. Biol. 13:7757-7765(1993).
RN 12
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RA Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mysdale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN 14
RP SEQUENCE FROM N.A.
RX STRAIN=B-6441;
RA MEDLINE=94016558; Pubmed=8411151;
RA Melnick L., Sherman F.;
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
RT of Saccharomyces cerevisiae share a common ancestry."
RL J. Mol. Biol. 233:372-388(1993).
CC - SUBCELLULAR LOCATION: Nuclear (Probable).
CC - SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
CC
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DR EMBL: L25428; AAL16070.1; -
DR EMBL: U18779; AAB65005.1; -
DR EMBL: L22172; AAA34935.1; -
DR EMBL: L22173; AAA34938.1; -
DR EMBL: S65964; AAD13972.1; -
DR EMBL: S66117; AAB28441.1; -
DR PIR: S30845; S30845.
DR HSSP: P54725; IDVO.
DR SGD: S0000763; RAD23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF00240; Ubiquitin; 1.
DR Pfam: PF00627; UBA; 2.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRfam: TIGR00601; rad23; 1.
DR PROSITE: PS00053; UBQUITIN_2; 1.
DR DNA damage; DNA repair; Nuclear protein.
FW DOMAIN 1 77 UBQUITIN-LIKE.
FT CONFLICT 277 77
SQ SEQUENCE 398 AA; 42366 MW; B3F0436DAB60B833 CRC64;

Query Match 21.18; Score 403; DB 1; Length 398;
Best Local Similarity 31.78; Pred. No. 7e-19;
Matches 130; Conservative 63; Mismatches 157; Indels 60; Gaps 16;

QY 1 MKLVKTLKGNHFEIRQPNDFITMAVK-KNIEIQGDSYWGQGLIFNCKVTKDESTL 59
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QY 60 EENKVNEDGFLVVMISKSGTSGTSSOSHNPATFQAPPLPAPQAA---POPPVAPI 116
Db 58 SEGGLKGDQYVFWVSQK---STKIKVTEPPIAPESATTPGGRNSTEASSTQASAPRA 114
QY 117 TT-----SOP-EGDPAQAPNTHDNAASNLLSGRNVDTIINQIMMGSGWMDKDYORALR 171
Db 115 ATAPEGSQPQEQATERTESASTPGFVGTERTETIERIMENG---YQREVERALRA 171
QY 172 AAYNPERAVEYLSGIPYTAELIAPVIGGAGANTTDRAPTGAGLSGIPNAPLDFQGA 231
Db 172 AFNNDRAVEYLLGIP--ENLRQPEPQOTAAAEDPSTAAATTAQDP--AEDDLFAQAA 227
QY 232 --SNAGGA---GGCPDLFLRNPP-----QFOAVREWHNPQILOPMLVELSKON 277
Db 228 QGGNASSGALGTGTGADDAAGCGPGSIGLVEEDLSIRQVSSGNPEALAPLENISARY 287
QY 278 POLRLLENNHDEFLQLINEP-----FEGG---EGDFLD-----OPEDEEM 315
Db 288 POLREHIANEVEYVSMLEAVGDNMODVMEGADDMVEGEDIETVGEAAAAGLQGGREG 347
QY 316 PHAIVSYPREBOEALIGRLESMPDRARYEAFACDRNEELIANYLLEHAGEED 364
Db 348 SFQYDLYTPEDDQASIRLCELFERDLYQVYFACDKNEELIANYLLEHAGEED 397

RESULT 7
YAUD_SCHPO STANDARD; PRT; 354 AA.
AC Q10169;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C26A3.16 in chromosome I.
GN SPAC26A3.16.
OS Schizosaccharomyces pombe (fission yeast).

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OC Eukaryota, Fungi: Ascomycota: Schizosaccharomycetes:
OC Schizosaccharomycetales: Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Crofton A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA Moore P., Moule S., Mungall K., Murphy L., Niblett D., Oell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Egger P., Zimmermann W., Wedler H., Wandut R., Purrelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Luga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: TO YEAST DSK2.
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
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CC -----
CC EMBL: 269240; CAA93239.1; -
CC InterPro: IPR000449; UBA_domain.
CC InterPro: IPR000626; Ubiqultin.
CC Pfam: PF00627; UBA.1.
CC Pfam: PF00627; UBA.1.
CC SMART: SM00165; UBA.1.
CC SMART: SM00213; UBO.1.
CC PROSITE: PS50053; UBIQUITIN_2; 1.
CC Hypothetical protein.
CC DOMAIN 1 78 UBIQUITIN-LIKE.
CC SEQUENCE 354 AA: 36819 MW: 1A99B2D97E73A831 CRC64:
SQ

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Query Match      8.6%; Score 163.5; DB 1; Length 354;
Best Local Similarity 22.7%; Pred. No. 0.0012;
Matches 95; Conservative 62; Mismatches 134; Indels 127; Gaps 21;

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OY 156 -----GGGSKDKKQVOR-ALRAAYNPDE--RAVEYL-----SGIPVTAETIAVPICGGGA 202
OY 174 SPLLRLNAPPYVRQMOSPEFFRRAMTBDTWRMAQLHQMGACIDPMISIMGGLGAGL 233
OY 203 NTTDRAPTGAGLSGIPNTAPLDFPOGASNAGG--AGGGPLDFLNNNPQFQAVREMYH 261
OY 234 -----GGLGGAGLGGF-----GGANNATAGTGAAPVD-----QTAAANTT--- 269
OY 262 NPQILQPMVLKSKNPQILRLIEHNHDEFQLNLE-----PFDGEGD-----F 306
OY 270 -----GNN-----LLNNGGAGFGAGLGDAGLGGAGGAS 299
OY 307 LDQPEDEMPHAISVPEEQ--EAIGLESMEF--DRARYTEAFACDRNEELANLYL 361
OY 300 PPAADPTTRP-----PEERYADQLSOLNMGCFVDEFRVQALRRSGVNOGATIESLL 351
DB
OY 307 LDQPEDEMPHAISVPEEQ--EAIGLESMEF--DRARYTEAFACDRNEELANLYL 361
OY 300 PPAADPTTRP-----PEERYADQLSOLNMGCFVDEFRVQALRRSGVNOGATIESLL 351
DB

```

RESULT 8

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DSK2_YEAST
ID DSK2_YEAST STANDARD; PRT; 373 AA.
AC P48510;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiqultin-like protein DSK2.
GN DSK2 OR SHE4 OR YMR276W OR YMR8021.02.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=962881973; PubMed=8682868;
RA Biggins S., Ivanovska I., Rose M.D.;
RT "Yeast ubiquitin-like genes are involved in duplication of the
RT microtubule organizing center.";
RL J. Cell Biol. 133:1331-1346(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
RL Submitted (May-1995) to the EMBL/GenBank/DDb databases.
CC -1- FUNCTION: INVOLVED, WITH RAD23 IN SPINDLE POLE BODY DUPLICATION.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: TO S.POMBE SPAC256A3.16.
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: L40587; AAB07267.1; -
CC EMBL: Z49704; CAA89774.1; -
CC HSSP: 015843; INDD.
CC SGD: S0004889; DSK2.
CC InterPro: IPR000449; UBA_domain.
CC InterPro: IPR000626; Ubiqultin.
CC Pfam: PF00240; ubiqultin; 1.
CC Pfam: PF00627; UBA.1.
CC SMART: SM00165; UBA.1.
CC SMART: SM00213; UBO.1.
CC PROSITE: PS00299; UBIQUITIN_1; 1.
CC PROSITE: PS50053; UBIQUITIN_2; 1.
CC Hypothetical protein.
CC DOMAIN 1 76 UBIQUITIN-LIKE.
CC FT CONFLICT 109 109 R -> A (IN REF. 2).
CC FT CONFLICT 296 296 R -> A (IN REF. 2).
CC FT SEQUENCE 373 AA: 39516 MW: 25EDF82B9DB67DF6 CRC64:
SQ

```



RA Guarino L.A.;  
RT "Identification of a viral gene encoding a ubiquitin-like protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:409-413(1990).  
RN [9]  
RP SEQUENCE FROM N.A.  
RC SPECIES-M.sexata;  
RA MEDLINE-91000673; PubMed-2169771;  
RX Schwartz L.M., Myer A., Kozs L., Engelstein M., Maier C.;  
RT "Activation of polyubiquitin gene expression during developmentally  
programmed cell death.";  
RL Neuron 5:411-419(1990).  
RN [10]  
RP SEQUENCE FROM N.A.  
RC SPECIES-M.sexata; TISSUE-Pupae;  
RX MEDLINE-91045065; PubMed-1700368;  
RA Bischoff S.T., Schwartz L.M.;  
RT "Characterization of a ubiquitin-fusion gene from the tobacco  
hawmoch, Manduca sexta.";  
RL Nucleic Acids Res. 18:6039-6043(1990).  
CC -I- FUNCTION: Involved in the ATP-dependent selective degradation of  
cellular proteins, the maintenance of chromatin structure, the  
regulation of gene expression, the stress response, and ribosome  
biogenesis.  
CC -I- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
CC -I- MISCELLANEOUS: Ubiquitin is synthesized as a polyubiquitin  
precursor with exact head to tail repeats, the number of repeats  
differs between species (up to 12 in Xenopus). In some species  
there is a final amino-acid after the last repeat. Some ubiquitin  
genes contain a single copy of ubiquitin fused to a ribosomal  
protein (either L40 or S27A).  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
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DR EMBL; M33013; AAA28999.1; -;  
DR EMBL; M33015; AAA29001.1; -;  
DR EMBL; M33122; AAA29007.1; -;  
DR EMBL; M22428; AAA28997.1; ALT\_TERM.  
DR EMBL; M22536; AAA28998.1; ALT\_TERM.  
DR EMBL; X53059; CAA37227.1; ALT\_TERM.  
DR EMBL; X59943; CAA42568.1; ALT\_TERM.  
DR EMBL; X69119; CAA48871.1; -;  
DR EMBL; AE003479; AAG22240.1; ALT\_TERM.  
DR EMBL; AE003479; AAG22241.1; ALT\_TERM.  
DR EMBL; AE003577; AAF51034.1; ALT\_TERM.  
DR EMBL; AE003628; AAF52941.1; ALT\_TERM.  
DR EMBL; M30306; AAA29989.1; ALT\_SEQ.  
DR EMBL; X53524; CAA37599.1; ALT\_TERM.  
DR PIR; A02575; UQPFM.  
DR PIR; B31560; UQPFM.  
DR PIR; B34813; UQPFM.  
DR PIR; S13136; UQO7A.  
DR PIR; A26087; A26087.  
DR PIR; A31560; A31560.  
DR PIR; JH0302; JH0302.  
DR PIR; S10319; S10319.  
DR PIR; S23988; S23988.  
DR FLYBase; FBgn0003941; RPL40.  
DR FLYBase; FBgn0003942; RPS27A.  
DR FLYBase; FBgn0003943; UBI-633E.  
DR InterPro; IPR000626; ubiquitin.  
DR PROSITE; PS00299; UBIQUITIN\_1; 1.  
DR PROSITE; PS50053; UBIQUITIN\_2; 1.  
KM Nuclear protein; Polyprotein.  
FT BINDING 54 54  
FT SITE 68 68  
NECESSARY FOR BRANCHED-CHAIN  
MULTIUBQUITIN ADDUCTS.  
CONJUGATION TO ACTIVATING ENZYME.  
ESSENTIAL FOR FUNCTION.

FT BINDING 72 72 CONJUGATION TO ACTIVATING ENZYME.  
FT BINDING 76 76 CONJUGATION TO ACCEPTOR PROTEINS.  
SQ SEQUENCE 76 AA; 8565 MW; CA2A35397EFD9B52 CRC64;  
Query Match 6.4%; Score 122.5; DB 1; Length 76;  
Best Local Similarity 40.5%; Pred. No. 0.065;  
Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;  
OY 1 MKLTVTKGTHPEIRNPNDTMAVKNEIEIQGDSYPMGQQLIFNGKVLKDESTLE 60  
DB 1 MQLFVTKLTGKTTLEVEPSDTIENK---AKIQDKEGIPDQQRILIFAGKQLQEDRTLS 57  
OY 61 ENKNEDGELVNL 74  
DB 58 DYNQKESTLHVL 71  
RESULT 10  
UBIQ\_HUMAN STANDARD; PRT; 76 AA.  
AC P02248; P02249; P02250; Q29120; Q91887; Q91888;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-ANG-1987 (Rel. 05, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ubiquitin.  
GN (UBA52 OR UBCEP2) AND UBB AND UBC AND (UBA80 OR UBCEP1 OR RPS27A).  
OS Homo sapiens (Human).  
OS Mus musculus (Mouse).  
OS Rattus norvegicus (Rat).  
OS Bos taurus (Bovine).  
OS Cavia porcellus (Guinea pig).  
OS Cricetus griseus (Chinese hamster).  
OS Onychomys longicaudatus (Long-tailed hamster) (Chinese hamster).  
OS Cricetulus cricetus (Rabbit).  
OS Sus scrofa (Pig).  
OS Gallus gallus (Chicken), and  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI TaxID=9606, 10090, 10116, 9913, 10141, 10029, 10030, 9986, 9823,  
OX 9031, 8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Human;  
RX MEDLINE-85230546; PubMed-2988935;  
RA Wdberg O., Pedersen M.S., Wind A., Berglund L.E., Marcker K.A.,  
RV Vuust J.;  
RT "The human ubiquitin multigene family: some genes contain multiple  
directly repeated ubiquitin coding sequences.";  
RL EMBO J. 4:755-759(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Human;  
RX MEDLINE-87326412; PubMed-2820408;  
RA Einspanner R., Sharma H.S., Schelt K.H.;  
RT "Cloning and sequence analysis of a cDNA encoding poly-ubiquitin in  
human ovarian granulosa cells.";  
RL Biochem. Biophys. Res. Commun. 147:581-587(1987).  
RN [3]  
RP SEQUENCE FROM N.A. (UBB).  
RC SPECIES-Human; TISSUE-Lymphocytes;  
RX MEDLINE-87146371; PubMed-3029682;  
RA Baker R.T., Board P.G.;  
RT "The human ubiquitin gene family: structure of a gene and pseudogenes  
from the UB B subfamily.";  
RL Nucleic Acids Res. 15:443-463(1987).  
RN [4]  
RP SEQUENCE FROM N.A. (UBA52).  
RC SPECIES-Human;  
RX MEDLINE-91212181; PubMed-1850507;  
RA Baker R.T., Board P.G.;  
RT "The human ubiquitin-52 amino acid fusion protein gene shares several  
structural features with mammalian ribosomal protein genes.";



RL Nucleic Acids Res. 19:1035-1040(1991).  
RN [5]  
RP SEQUENCE OF 5-76 FROM N.A. (UBA80).  
RC SPECIES-Human;  
RX MEDLINE-85207809; PubMed-2581967;  
RA Lund P.K., Moats-Staats B.M., Simmons J.G., Hoyt E., D'Ercole A.J.,  
RA Martin F., van Wyk J.O.;  
RT "Nucleotide sequence analysis of a cDNA encoding human ubiquitin  
RT reveals that ubiquitin is synthesized as a precursor.";  
RL J. Biol. Chem. 260:7609-7613(1985).  
RN [6]  
RP SEQUENCE OF 1-74.  
RC SPECIES-Human;  
RX MEDLINE-75156547; PubMed-124018;  
RA Schlesinger D.H., Goldstein G.;  
RT "Hybrid tropomyosin reconstituted from vertebrate and arthropod  
RT subunits.";  
RL Nature 255:423-424(1975).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse; STRAIN-C57BL/6;  
RX MEDLINE-90245601; PubMed-2159627;  
RA Finch J.S., Bonham K., Kriegl P., Bowden G.T.;  
RT "Murine polyubiquitin mRNA sequence.";  
RL Nucleic Acids Res. 18:1907-1907(1990).  
RN [8]  
RP SEQUENCE.  
RC SPECIES-Rat; STRAIN-Wistar; TISSUE-Duodenum;  
RX MEDLINE-94304928; PubMed-8031840;  
RA Hubbard M.J., Carne A.;  
RT "Differential feeding-related regulation of ubiquitin and  
RT calbindin9kda in rat duodenum.";  
RL Biochim. Biophys. Acta 1200:191-196(1994).  
RN [9]  
RP SEQUENCE FROM N.A. (UBA52).  
RC SPECIES-Rat; STRAIN-Sprague-Dawley;  
RX MEDLINE-96011832; PubMed-7488009;  
RA Chan Y.-L., Suzuki K., Wool I.G.;  
RT "The carboxyl extensions of two rat ubiquitin fusion proteins are  
RT ribosomal proteins s27a and l40.";  
RL Biochem. Biophys. Res. Commun. 215:682-690(1995).  
RN [10]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Bovine; TISSUE-Seminal vesicle;  
RX MEDLINE-93176814; PubMed-8382528;  
RA Wempe F., Scheit K.H.;  
RT "Characterization of a full-length cDNA encoding a bovine four  
RT tandem-repeat ubiquitin.";  
RL Biochim. Biophys. Acta 1172:209-211(1993).  
RN [11]  
RP SEQUENCE OF 1-74.  
RC SPECIES-Bovine;  
RX MEDLINE-75205496; PubMed-1170880;  
RA Schlesinger D.H., Goldstein G., Miall H.D.;  
RT "The complete amino acid sequence of ubiquitin, an adenylate cyclase  
RT stimulating polypeptide probably universal in living cells.";  
RL Biochemistry 14:2214-2218(1975).  
RN [12]  
RP SEQUENCE OF 1-50.  
RC SPECIES-Bovine;  
RX MEDLINE-81062406; PubMed-6254502;  
RA Hamilton J.W., Rouse J.B.;  
RT "The biosynthesis of ubiquitin by parathyroid gland.";  
RL Biochem. Biophys. Res. Commun. 96:114-120(1980).  
RN [13]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Pig;  
RX MEDLINE-88054463; PubMed-2821415;  
RA Einspanier R., Sharma H.S., Scheit K.H.;  
RT "An mRNA encoding poly-ubiquitin in porcine corpus luteum:  
RT identification by cDNA cloning and sequencing.";  
RL DNA 6:395-400(1987).  
RN [14]

RP SEQUENCE FROM N.A.  
RC SPECIES-C.porcillus; TISSUE-Spleen;  
RA Tsukagoshi N.;  
RT "Ascorbate-dependent expression of ubiquitin genes in guinea pig.";  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RP SEQUENCE FROM N.A.  
RC SPECIES-C.griseus; STRAIN-V79; TISSUE-Lung fibroblast;  
RX MEDLINE-9222105; PubMed-1314094;  
RA Nenoi M., Mita K., Ichimura S.;  
RT "Evolutionarily conserved structure of the 3' non-translated region  
RT of a Chinese hamster polyubiquitin gene";  
RL Biochim. Biophys. Acta 1150:247-252(1992).  
RN [16]  
RP SEQUENCE FROM N.A.  
RC SPECIES-C.longicaudatus; STRAIN-V79; TISSUE-Lung fibroblast;  
RX MEDLINE-89160248; PubMed-2537950;  
RA Fornace A.J. Jr., Alamo I. Jr., Hollander M.C., Lamoreaux E.;  
RT "Ubiquitin mRNA is a major stress-induced transcript in mammalian  
RT cells.";  
RL Nucleic Acids Res. 17:1215-1230(1989).  
RN [17]  
RP SEQUENCE.  
RC SPECIES-Rabbit; TISSUE-Brain;  
RX MEDLINE-93149997; PubMed-1337207;  
RA Wajih N., Siddiqi A.R., Kaiser R., Persson B., Zaidi Z.H.,  
RT Joernvall H.;  
RL "Structural characterization of rabbit brain ubiquitin.";  
RN Protein Seq. Data Anal. 5:31-32(1992).  
RN [18]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Chicken;  
RX MEDLINE-85213498; PubMed-2987683;  
RA Bond U., Schlesinger M.J.;  
RT "Ubiquitin is a heat shock protein in chicken embryo fibroblasts.";  
RL Mol. Cell. Biol. 5:949-956(1985).  
RN [19]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Chicken;  
RX MEDLINE-87089821; PubMed-3025663;  
RA Bond U., Schlesinger M.J.;  
RT "The chicken ubiquitin gene contains a heat shock promoter and  
RT expresses an unstable mRNA in heat-shocked cells.";  
RL Mol. Cell. Biol. 6:4602-4610(1986).  
RN [20]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Chicken; TISSUE-Spermatid;  
RX MEDLINE-8908351; PubMed-2850543;  
RA Mezquita J., Pau W., Mezquita C.;  
RT "cDNA encoding a chicken ubiquitin-fusion protein identical to the  
RT corresponding human protein.";  
RL Nucleic Acids Res. 16:11838-11838(1988).  
RN [21]  
RP SEQUENCE FROM N.A.  
RC SPECIES-X.laevis;  
RX MEDLINE-85048942; PubMed-6209017;  
RA Dworkin-Rasli E., Shrutkowski A., Dworkin M.B.;  
RT "Multiple ubiquitin mRNAs during Xenopus laevis development contain  
RT tandem repeats of the 76 amino acid coding sequence.";  
RL Cell 39:321-325(1984).  
RN [22]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RC SPECIES-Human;  
RX MEDLINE-87311725; PubMed-3041007;  
RA Vijay-Kumar S., Bugg C.E., Cook W.J.;  
RT "Structure of ubiquitin refined at 1.8-A resolution.";  
RL J. Mol. Biol. 194:531-544(1987).  
RN [23]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RC SPECIES-Human;  
RX MEDLINE-94220022; PubMed-8166633;  
RA Ramage R., Green J., Muir T.W., Ogunjobi O.M., Love S., Shaw K.;  
RT "Synthetic, structural and biological studies of the ubiquitin system:

Query Match 6.4%; Score 122.5; DB 1; Length 76;  
Best Local Similarity 40.5%; Pred. No. 0.065;  
Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;

1 MLKLVTELTGTHPEIRHVNNDITIMAYKKNIEEIKGDSYPMWGQOLLIFNGKYLKDSSTLE 60  
1 MOIFPKVTLTGKTTTLEVEVDITENYK---AKIQKKGIPPDQRLIFAGKOLEDRITLS 57

61 ENKVNEDGFVYVNL 74  
58 DYNQKESLHLVL 71

RESULT 11  
ID RFX1\_HUMAN STANDARD; PRT; 979 AA.  
AC P22670;  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE MHC class II regulatory factor RFX1 (RFX) (Enhancer factor C) (EF-C).  
GN RFX1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91071581; PubMed=2253877;  
RA Reith W., Sanchez-Herrero C., Kober M., Silacci P., Bette C.,  
RA Barras E., Mach B.;  
RT "MHC class II regulatory factor RFX has a novel DNA-binding domain  
and a functionally independent dimerization domain.";  
RL Genes Dev. 4:1528-1540(1990).  
RN [2]  
RP IDENTITY BETWEEN RFX1 AND EF-C.  
RX MEDLINE=94019311; PubMed=8413236;  
RA Siegrist C.A., Durand B., Emery P., David E., Hearing P., Mach B.,  
RA Reith W.;  
RT "RFX1 is identical to enhancer factor C and functions as a  
transactivator of the hepatitis B virus enhancer.";  
RL Mol. Cell. Biol. 13:6375-6384(1993).  
RN [3]  
RP BINDING TO RPL30 PROMOTER.  
RX MEDLINE=94040774; PubMed=8224874;  
RA Saitany G., Perry R.P.;  
RT "Transcription factor RFX1 helps control the promoter of the mouse  
ribosomal protein-encoding gene rpl30 by binding to its alpha  
element.";  
RL Gene 132:279-283(1993).  
RN [4]  
RP SHOWS THAT BLS IS NOT DUE TO RFX1.  
RX MEDLINE=92375076; PubMed=1508204;  
RA Sanchez-Herrero C., Reith W., Silacci P., Mach B.;  
RT "The DNA-binding defect observed in major histocompatibility complex  
class II regulatory mutants concerns only one member of a family of  
class II regulatory binding to the X boxes of class II promoters.";  
RL Mol. Cell. Biol. 12:4076-4083(1992).  
CC -1- FUNCTION: REGULATORY FACTOR ESSENTIAL FOR MHC CLASS II GENE  
EXPRESSION. BINDS TO THE X BOXES OF MHC CLASS II GENES. ALSO BINDS  
TO AN INVERTED REPEAT (ENH) REQUIRED FOR HEPATITIS B VIRUS GENES  
EXPRESSION AND TO THE MOST UPSTREAM ELEMENT (ALPHA) OF THE RPL30  
PROMOTER.  
CC -1- SUBUNIT: BINDS DNA AS AN HOMODIMER.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE RFX FAMILY.  
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-----  
DR EMBL: X58964; CAA41730.1; -  
DR EMBL: A20498; CAA01506.1; -  
DR PIR: A35913; A35913.  
DR TRANSFAC: T00909; -  
DR TRANSFAC: T01673; -  
DR GeneW: HGNC:9982; RFX1.  
DR MIM: 600006; -  
DR InterPro: IPR003150; RFX\_DNA\_binding.  
DR Pfam: PF02257; RFX\_DNA\_binding; 1.  
KW DNA-binding; Transcription regulation; Activator; Nuclear protein.  
FT DNA\_BIND 381 411 GLY-RICH.  
FT DOMAIN 438 528 EXPERIMENTALLY DEDUCED.  
FT DOMAIN 920 936 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 744 979 NECESSARY FOR DIMERIZATION.  
SQ SEQUENCE 979 AA; 104728 MW; 556151F8C6AC9A2 CRC64;

Query Match 6.4%; Score 122; DB 1; Length 979;  
Best Local Similarity 25.8%; Pred. No. 1.9;  
Matches 48; Conservative 31; Mismatches 75; Indels 32; Gaps 10;

75 SKGKTSGS--TGTSSSQ-----HSNTPARQAPPLAPQAPQP--PVAFITTS--QPEGL 124  
216 SSSKTAGAPRTGIVPQQLQVGVQOVSVPVQERSVQATQAPKPGVQPLTVQGLQPVHV 275  
125 PAQAPETHDMAASNLISGNVDITINQLMEMGSGSWDKKQVORALRAA--YNNPE----- 177  
276 AGEVQOQLQVPPVPHYS-----SQVQVEEG--DASTYASATSSSYSPPEPLTYQ 325  
178 RAVEYLSCIPVTAETAVPIGGGANTTDRAPTGEAGLSGIPNTPALDLPFGASNA--G 235  
326 TASTSYEAAGTATQVSTPATQAVASGSMPIVYSGQVVASASTG--AGASNSGG 382

236 GGAGCG 241  
383 GGSGGG 388

RESULT 12  
NED8\_HUMAN  
ID NED8\_HUMAN STANDARD; PRT; 81 AA.  
AC Q15843;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ubiquitin-like protein NED8.  
GN NED8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TTSUE-Fibrosarcoma;  
RX MEDLINE=98361870; PubMed=9694792;  
RA Osaka F., Kawasaki H., Aida N., Saeki M., Chiba T., Kawashima S.,  
RA Tanaka K., Kato S.;  
RT "A new NED8-ligating system for cullin-4A.";  
RL Genes Dev. 12:2263-2268(1998).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
RX MEDLINE=99074275; PubMed=9857030;  
RA Whidby F.G., Xia G., Pickart C.M., Hill C.P.;  
RT "Crystal structure of the human ubiquitin-like protein NED8 and  
interactions with ubiquitin pathway enzymes.";  
RL J. Biol. Chem. 273:34983-34991(1998).  
CC -1- FUNCTION: ACTIVATED BY AN E1-LIKE COMPLEX, CONSISTING OF APP-B1  
AND UBA3 AND THEN LINKED TO THE E2-LIKE ENZYME, UBC12. THE MAJOR  
CC TARGET PROTEIN MODIFIED BY NED8 IS CULLIN-4A.  
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE DURING THE EMBRYONIC  
CC DEVELOPMENT AND DIFFERENTIATION OF THE CENTRAL NERVOUS SYSTEM. MAY



FT BINDING 76 76 CONJUGATION TO ACCEPTOR PROTEINS.  
SQ SEQUENCE 76 AA: 8551 MW: C59A35397ERC9B53 CRC64;

Query Match 6.3%; Score 120.5; DB 1; Length 76;  
Best Local Similarity 40.5%; Pred. No. 0.088;  
Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;

OY 1 MKLTVKTLKGTHFEIRVQNDITMAVKKNIEIQGKDSYPMGQQLIFNGKYLKDESTLE 60  
DB 1 MQLFVKTLGKTIITLDEPSDIENVK--AKIQDEKGIIPDQRLIFAGKQLEDGRTLS 57  
OY 61 ENKVNEDGFLVYML 74  
DB 58 DYNIOKESTLHLVL 71

RESULT 15

UBIQ\_LEIMA STANDARD; PRT; 76 AA.  
AC Q05550.  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Ubiquitin.  
OS Leishmania major.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MHOM/IR/83/LIT252;  
RX MEDLINE=93380668; PubMed=8396548;  
RA Graeff G.R., Steele P.M., Peterson C.L., Bennett M.L., Langer P.J.;  
RT "Sequence of a Leishmania major gene encoding an ubiquitin fusion  
protein.";  
RL Gene 131:155-156(1993).  
CC -! FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF  
CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE  
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME  
BIogenesis.  
CC -! SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
CC -! MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED WITH RIBOSOMAL CEP52 AS  
ITS C-TERMINAL EXTENSION.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; 214232; CAA78598.1; -.  
DR HSSP; P02248; IUBI.  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00240; ubiquitin; 1.  
DR PRINTS; PR00348; UBQUITIN.  
DR SMART; SM00213; UBQ; 1.  
DR PROSITE; PS00299; UBQUITIN\_1; 1.  
DR PROSITE; PS50053; UBQUITIN\_2; 1.  
KW Nuclear protein; Polypeptide.  
FT SITE 48  
FT 48  
FT BINDING 76  
SQ SEQUENCE 76 AA: 8549 MW: C52648497FFD8E47 CRC64;

Query Match 6.2%; Score 118.5; DB 1; Length 76;  
Best Local Similarity 39.2%; Pred. No. 0.12; Mismatches 27; Indels 3; Gaps 1;

OY 1 MKLTVKTLKGTHFEIRVQNDITMAVKKNIEIQGKDSYPMGQQLIFNGKYLKDESTLE 60  
DB 1 MQLFVKTLGKTIITLDEPSDIENVK--AKIQDEKGIIPDQRLIFAGKQLEDGRTLS 57

OY 61 ENKVNEDGFLVYML 74  
DB 58 DYNIOKESTLHLVL 71  
Search completed: November 4, 2002, 02:00:37  
Job time : 15.806 secs